

SEQUENCE LISTING

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Belcourt, M.

<120> COMPOSITIONS AND METHODS FOR
TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES

<130> 8002-059

<150> 60/157,581

<151> 1999-10-04

<150> 60/157,637

<151> 1999-10-04

<160> 61

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward primer

<400> 1

gaagatcttc cggaggaggg gaaatg

26

<210> 2

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer

<400> 2

cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc

44

<210> 3

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(474)

<400> 3

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Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1 5 10 15

48

gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt	96
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag	144
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg	192
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc	240
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc	288
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	
gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg	336
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag	384
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	
aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat	432
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	
ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg	474
Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu	
145 150 155	
taa	477

<210> 4
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His	
1 5 10 15	
Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg	
20 25 30	
Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln	
35 40 45	
Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu	
50 55 60	
Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr	
65 70 75 80	
Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser	
85 90 95	
Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala	
100 105 110	
Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu	
115 120 125	
Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp	
130 135 140	

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 5
 ccgacgcgtt gacacctgaa aactggag

28

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer

<400> 6
 ccgacgcgtg aaaggatctc aagaagatc

29

<210> 7
 <211> 543
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(540)

<400> 7
 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15

48

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc
 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
 20 25 30

96

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag
 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
 35 40 45

144

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
 50 55 60

192

gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
 65 70 75 80

240

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
 85 90 95

288

gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc	336
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr	
100 105 110	
aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act	384
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr	
115 120 125	
ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt	432
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly	
130 135 140	
ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac	480
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn	
145 150 155 160	
cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt	528
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly	
165 170 175	
att atc gca ctg taa	543
Ile Ile Ala Leu	
180	

<210> 8
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 8	
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala	
1 5 10 15	
Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser	
20 25 30	
Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln	
35 40 45	
Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val	
50 55 60	
Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu	
65 70 75 80	
Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His	
85 90 95	
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr	
100 105 110	
Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr	
115 120 125	
Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly	
130 135 140	
Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn	
145 150 155 160	
Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly	
165 170 175	
Ile Ile Ala Leu	
180	

<210> 9
 <211> 801
 <212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(798)

<400> 9
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Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15
acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
20 25 30
aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
35 40 45
tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
50 55 60
gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65 70 75 80
tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
85 90 95
ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
100 105 110
ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
115 120 125
gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
130 135 140
ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc 480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145 150 155 160
atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga 528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
165 170 175
ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc 576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
180 185 190
caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg 624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
195 200 205

aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc	672
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu	
210 215 220	
tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga	720
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg	
225 230 235 240	
att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa	768
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu	
245 250 255	
gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa	801
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly	
260 265	

<210> 10
 <211> 266
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 10	
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala	
1 5 10 15	
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp	
20 25 30	
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser	
35 40 45	
Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln	
50 55 60	
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr	
65 70 75 80	
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser	
85 90 95	
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr	
100 105 110	
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn	
115 120 125	
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser	
130 135 140	
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val	
145 150 155 160	
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg	
165 170 175	
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val	
180 185 190	
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met	
195 200 205	
Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu	
210 215 220	
Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg	
225 230 235 240	
Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu	
245 250 255	
Ala Ser Phe Phe Gly Ala Phe Leu Val Gly	
260 265	

<210> 11
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(462)

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    <400> 11
atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act      48
Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
  1              5              10              15

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa      96
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
              20              25              30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc      144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
              35              40              45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa      192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
              50              55              60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg      240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
              65              70              75              80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct      288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
              85              90              95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta      336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
              100              105              110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac      384
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
              115              120              125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc      432
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
              130              135              140

ttt gcc caa tcg atc att agc acg tta act taa      465
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145              150

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<210> 12
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 12
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1 5 10 15
Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln
20 25 30
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
35 40 45
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
50 55 60
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
65 70 75 80
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
85 90 95
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
100 105 110
Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
115 120 125
Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
130 135 140
Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
145 150

<210> 13
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Fusion construct

<221> CDS
<222> (1)...(462)

<400> 13
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Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr 15
1 5 10
agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa 96
Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln 20 25 30
ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc 144
Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly 35 40 45
atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192
Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys 50 55 60
ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg 240
Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu 65 70 75 80
gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288
Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser 85 90 95
aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336
Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val 100 105 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140

ttt gcc caa tcg atc att agc acg tta act taa 465
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 14
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 14
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 35 40 45
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 100 105 110
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 15
 agtctagaca atcaggcgaa gaacgg

26

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer

<400> 16	25
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<210> 17	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 17	31
ggatccttaa gaccacttt cacatttaag t	
<210> 18	
<211> 28	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Reverse primer	
<400> 18	28
ggttccatgg ttcacttttc tctatcac	
<210> 19	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 19	33
gtgtccatgg ggcacagcca ccgcgacttc cag	
<210> 20	
<211> 34	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Reverse primer	
<400> 20	34
acacgagctc ctacttgag gcagtcatga agct	
<210> 21	
<211> 72	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Forward primer	
<400> 21	60
gtgtccatgg ctcggcgggc aagtgtcggg actgaccatc atcatcatca tcatcacagc	72
caccgagct tc	
<210> 22	
<211> 35	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Reverse primer

<400> 22 35
gtgcggatcc ctacttggag gcagtcatga agctg

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His
1 5 10 15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>

<223> Peptide sequence TiP 13.40

<400> 24
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
1 5 10 15
Val Val Met Tyr Glu Gly
20

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleotide sequence encoding TiP13.40

<400> 25 60
gcgtaccgct ggcgcctgtc ccacgcgccg aaaaccggct ttatccgcgt ggtgatgtac 66
gaaggc

<210> 26
<211> 101
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 26 60
gtgtactagt gtggcgcagg cggcgtaccg ctggcgcctg tcccatcgcc cgaaaaccgg 101
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c

<210> 27
<211> 101
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 27
 gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccgggttttc gggcgatggg 60
 acaggcgcca gcggtacgcc gcctgcgcca cactagtaca c 101

<210> 28
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
 1 5 10 15
 Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
 20 25 30
 Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
 35 40 45
 Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
 50 55 60
 Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
 65 70 75 80
 Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
 85 90 95
 Lys Leu Leu Glu Ser
 100

<210> 29
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 29
 cttcactagt gtggcgagg cgaacggccg caaaatctgc ctggacctgc aggcgccgct 60
 gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg 106

<210> 30
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 30
 cgcgatcct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag 60
 gtccaggcag attttgcggc cgttcgctg cgccacacta gtgaag 106

<210> 31
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 31
 Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
 1 5 10 15
 Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
 20 25 30
 Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
 35 40 45

Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
 50 55 60
 Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met
 65 70 75 80
 Thr Asp Ala Arg Lys
 85

<210> 32
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 32
 ggcttcacta gtgtggcgca ggcgatatac tcctttgatg gtcg

44

<210> 33
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 33
 cgcggatcct tacttcctag cgtctgtcat gaaactg

37

<210> 34
 <211> 7117
 <212> DNA
 <213> E. coli

<400> 34
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Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
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ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc 144
Pro Pro Thr Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
35 40 45

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 Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
 80 85 90
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 Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
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 Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
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Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
35 40 45

ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc 192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
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Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
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Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
80 85 90

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Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
95 100 105 110

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Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr
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Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser
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Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr
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Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser
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